L Number	Hits	Search Text	DB	Time stamp
1	50138	test adj1 sample or cell near5 mRNa	USPAT;	2003/11/06 16:26
			US-PGPUB;	
			DERWENT	
2	24345	(test adj1 sample or cell near5 mRNa) and	USPAT;	2003/11/06 16:41
_		compound	US-PGPUB;	
		<u>-</u>	DERWENT	
3	9991	((test adj1 sample or cell near5 mRNa) and	USPAT;	2003/11/06 16:41
	333-	compound) and gene adj1 expression	US-PGPUB;	
		compound, and gone dage employees	DERWENT	
4	0	(((test adj1 sample or cell near5 mRNa)	USPAT;	2003/11/06 16:42
3		and compound) and gene adj1 expression)	US-PGPUB;	2000, 22, 00 20112
		and apoptpsis	DERWENT	
5	9231	(((test adj1 sample or cell near5 mRNa)	USPAT;	2003/11/06 16:42
)	9231	and compound) and gene adjl expression)	US-PGPUB;	2003/11/00 10.42
ا ا	5000	and hybridization	DERWENT	2002/11/06 16:43
6	5330	((((test adj1 sample or cell near5 mRNa)	USPAT;	2003/11/06 16:43
		and compound) and gene adj1 expression)	US-PGPUB;	
		and hybridization) and array	DERWENT	0000/11/06 16 40
7	2350	((((test adj1 sample or cell near5 mRNa)	USPAT;	2003/11/06 16:43
		and compound) and gene adj1 expression)	US-PGPUB;	
		and hybridization) and array) and signal	DERWENT	
		adj1 transduction		
8	1714	(((((test adj1 sample or cell near5 mRNa)	USPAT;	2003/11/06 16:44
		and compound) and gene adj1 expression)	US-PGPUB;	
		and hybridization) and array) and signal	DERWENT	
		adj1 transduction) and differential		
9	1456	((((((test adj1 sample or cell near5	USPAT;	2003/11/06 16:50
		mRNa) and compound) and gene adj1	US-PGPUB;	
		expression) and hybridization) and array)	DERWENT	
		and signal adj1 transduction) and		
		differential) and display		
10	2044	differential adj1 display	USPAT;	2003/11/06 16:50
			US-PGPUB;	
			DERWENT	
11	1824	(differential adj1 display) and mRNA	USPAT;	2003/11/06 16:50
		(,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	US-PGPUB;	
			DERWENT	
12	7918	((differential adj1 display) and mRNA)	USPAT;	2003/11/06 16:50
	, , , , ,	microarray	US-PGPUB;	=====================================
		microarray	DERWENT	
13	. 370	((differential adj1 display) and mRNA) and	USPAT;	2003/11/06 16:50
13	370	microarray	US-PGPUB;	2003/11/00 10:30
		microarray	DERWENT	
1	0	///differential add displays and mDNAS	USPAT;	2003/11/06 16:51
14	U	(((differential adj1 display) and mRNA)		2003/11/00 10.31
		and microarray) and endocrine adj1	US-PGPUB; DERWENT	}
1	_	disruptor		2002/11/06 16:51
15	0		USPAT;	2003/11/06 16:51
		and microarray) and gene adj1 disruptor	US-PGPUB;	
		],,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	DERWENT	0000/11/06 16 50
16	155		USPAT;	2003/11/06 16:52
		and microarray) and apoptosis	US-PGPUB;	
			DERWENT	]

09/830,652

- L2 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2002 ACS
- AN 1996:735364 CAPLUS
- DN 126:15256
- TI Use of a cDNA microarrays to analyze gene expression patterns in human cancer
- AU DeRisi, Joseph; Penland, Lolita; Brown, Patrick O.; Bittnber, Michael L.; Meltzer, Paul S.; Ray, Michael; Chen, Yidong; Su, Yan A.; Trent, Jeffrey M.
- CS Howard Hughes Medican Inst., Stanford Univ., Stanford, CA, 94305, USA
- SO Nature Genetics (1996), 14(4), 457-460
- CODEN: NGENEC; ISSN: 1061-4036 PB Nature Publishing Co.
- PB Nature P DT Journal
- LA English
- The development and progression of cancer1-3 and the exptl. reversal of AΒ tumorigenicity4,5 are accompanied by complex changes in patterns of gene expression. Microarrays of cDNA provide a powerful tool for studying these complex phenomena. The tumorigenic properties of a human melanoma cell line, UACC-903, can be suppressed by introduction of a normal human chromosome 6, resulting in a redn. of growth rate, restoration of contact inhibition, and suppression of both soft agar clonogenicity and tumorigenicity in nude mice. We used a high d. microarray of 1,161 DNA elements to search for differences in gene expression asseed. with tumor suppression in this system. Fluorescent probes for hybridization were derived from two sources of cellular mRNA [UACC-903 and UACC-903(+6)] which were labeled with different fluors to provide a direct and internally controlled comparison of the mRNA levels corresponding to each arrayed gene. The fluorescence signals representing hybridization to each arrayed gene were analyzed to det. the relative abundance in the two samples of mRNAs corresponding to each gene. Previously unrecognized alterations in the expression of specific genes provide leads for further investigation of the genetic basis of the tumorigenic phenotype of the genetic basis of the tumorigenic phenotype of these cells.